SEQUENCE LISTING

5	(1) GENE	RAL INFORMATION:
	(i)	APPLICANTS: Liu, Qingyun Chen, Fang
10	(ii)	TITLE OF INVENTION: Human Uncoupling Protein 3
10	(iii)	NUMBER OF SEQUENCES: 21
15	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Merck & Co., Inc. (B) STREET: P.O. Box 2000 RY60-30 (C) CITY: Rahway (D) STATE: NJ (E) COUNTRY: US
20		(F) ZIP: 07065-0907
20	(v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible
25		(C) OPERATING SYSTEM: PC-DOS/MS-DOS(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
30	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE: (C) CLASSIFICATION:
35	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Hand, J. Mark (B) REGISTRATION NUMBER: 36,545 (C) REFERENCE/DOCKET NUMBER: 19959Y
40	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 732/594-3905 (B) TELEFAX: 732/594-4720
	(2) INFO	RMATION FOR SEQ ID NO:1:
45	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 404 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
50	(::)	MOLECULE MUDE. ADNA

55

	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:I:	
	GGTGACCTAC GACATCCTCA AGGAGAAGCT GCTGGACTAC CACCTGCTCA CTGACAACTT	. 60
5	CCCCTGCCAC TTTGTCTCTG CCTTTGGAGC CGGCTTCTGT GCCACAGTGG TGGCATCCCC	120
	GGTGGACGTG GTGAAGACCC GGTATATGAA CTCACCTCCA GGCCAGTACT TCAGCCCCCT	180
10	CGACTGTATG ATAAAGATGG TGGCCCAGGA GCGCCACCAG CCTTCTACAA GGGATTTACA	240
10	CCCTCCTTTT TGCGTTTGGG ATCCTGGAAC GTGGTGATGT TCGTAACCTA TGAGCAGCTG	300
	AAACGGGCCC TGATGAAAGT CCAGATGTTA CGGGAATCAC CGTTTTGAAC AAGACAAGAA	360
15	GGCCACTGGT AGCTAACGTG TCCGAAACCA GTTAAGAATG GAAG	404
	(2) INFORMATION FOR SEQ ID NO:2:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 405 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(ii) MOLECULE TYPE: cDNA	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
,	GGTGACCTAC GACATCCTCA AGGAGAAGCT GCTGGACTAC CACCTGCTCA CTGACAACTT	60
	CCCCTGCCAC TTTGTCTCTG CCTTTGGAGC CGGCTTCTGT GCCACAGTGG TGGCATCCCC	120
35	GGTGGACGTG GTGAAGACCC GGTATATGAA CTCACCTCCA GGCCAGTACT TCAGCCCCCT	180
	CGACTGTATG ATAAAGATGG TGGCCCAGGA GCGCCACCAG CCTTCTACAA GGGATTTACA	240
40	CCCTCCTTNT TTGCGTTTGG GATCCTGGAA CGTGGTGATG TTCGTAACCT ATGAGCAGCT	300
	GAAACGGGCC CTGATGAAAG TCCAGATGTT ACGGGAATCA CCGTTTTGAA CAAGACAAGA	360
	AGGCCACTGG TAGCTAACGT GTCCGAAACC AGTTAAGAAT GGAAG	405
15	(2) INFORMATION FOR SEQ ID NO:3:	
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 159 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	

	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
5	CGAGCAGCTG AAACGGGCCC TGATGAAAGT CCAGATGTTA CGGGNATCAC CGTTTTGAAC	60
J	AAGACAAGAA GGCCACTGGT AGCTAACGTN TCCGAAACCA GTTAAGATTG GAAGAAAACG	120
	GTCCATCCAC GNACACATGG ACACAGACCC ACACATNTT	159
10	(2) INFORMATION FOR SEQ ID NO:4:	
15	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 484 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
25	TTTTTTTGT TCTTACTCCC ACACCTAAGG TGGAANTTCT TTTATTGAGT CATAATAATT	60
	TCCCGAGAAT TCCGAGTCCT GCTACTTTAG GTTCTTGCCC AGGAATCCAC CTCTTTTCCC	120
30	CCAAGCCCAA CAATCCTTTG AGGTACTCAT GATTGAGCGC GTGGTGGGGG GGGGTGGGGA	180
30	AGAGGCTGCA TGGGGGTGGG GCTCCTGTGG CTTCACGTCA TCCACTGTCA CCTCTGGTCC	240
	CCAAGTCTCT GGATCCTTTG GTCTCACCTC TAGACAACCG GCGGGGTTCA AACCTTCTTC	300
35	CCTGGCAACT CCTCTCTGTC CCGACAAAAT CTCTCCCAAG GCATTGTCCT TGTAGTTAGA	360
	TTTACACAGA GCTTTTGCTT TTATAAAGTG CGTTCATGCC CAGCTTCTCA CTTGCATGTC	420
40	ATAGCACCCC TGGTGAGGTG GACAGGGAAG GGATGGCTCC CTCCATTTTG TAGGAAAGTN	480
	GGGG	484
	(2) INFORMATION FOR SEQ ID NO:5:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	

46-

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
	AAGCTGCTGG ACTACCACCT GCTC	24
5	(2) INFORMATION FOR SEQ ID NO:6:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
15	<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"</pre>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	TACTGCCCTG GAGGTGAGTT CA	22
	(2) INFORMATION FOR SEQ ID NO:7:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	
30	<pre>(D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid</pre>	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
40	CCAAGCCCAA CAATCCTTTG A	21
	(2) INFORMATION FOR SEQ ID NO:8:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
50	<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"</pre>	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	



	CCAAAGGATC CAGAGACTTG G	21
	(2) INFORMATION FOR SEQ ID NO:9:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single 	
10	(D) TOPOLOGY: linear	
-0	<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"</pre>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
	TTGTGTGGAA TTGTGAGCGG ATAAC	25
20	(2) INFORMATION FOR SEQ ID NO:10:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
30	<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"</pre>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
	CCAGGGTTTT CCCAGTCACG AC	22
40	(2) INFORMATION FOR SEQ ID NO:11:	
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 2340 base pairs(B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
73		
	(ii) MOLECULE TYPE: cDNA	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
	TCGAACTCAC TCACCTCCCC TCTCACCTCA CTGCCCTCAC CAGCCAGCCT CTTGTCAAGT	60
55	GATCAGGCTG TCAACCAACT TCTCTAGGAT AAGGTTTCAG GTCAGCCTGT GTGTATAAGA	120

CCAGTGCCAA GCCAGAAGCA GCAGAGACAA CAGTGAATGA CAAGGAGGGG CCATCCAATC 180 CCTGCTGCCA CCTCCTGGGA TGGAGCCCTA GGGAGCCCCT GTGCTGCCCC TGCCGTGGCA 240 5 GGACTCACAG CCCCACCGCT GCACTGAAGC CCAGGGCTGT GGAGCAGCTC TCTCCTTGGA 300 CTCCTCTCGG CCCTAAAGGG ACTGGGCAGA GCCTTCCAGG ACTATGGTTG GACTGAAGCC 360 10 TTCAGACGTG CCTCCCACCA TGGCTGTGAA GTTCCTGGGG GCAGGCACAG CAGCCTGTTT 420 TGCTGACCTC GTTACCTTTC CACTGGACAC AGCCAAGGTC CGCCTGCAGA TCCAGGGGGA 480 GAACCAGGCG GTCCAGACGG CCCGGCTCGT GCAGTACCGT GGCGTGCTGG GCACCATCCT 540 15 600 GACCATGGTG CGGACTGAGG GTCCCTGCAG CCCCTACAAT GGGCTGGTGG CCGGCCTGCA GCGCCAGATG AGCTTCGCCT CCATCCGCAT CGGCCTTTAC GACTCCGTCA AGCAGGTGTA 660 20 CACCCCAAA GGCGCGGACA ACTCCAGCCT CACTACCCGG ATTTTGGCCG GCTGCACCAC 720 AGGAGCCATG GCGGTGACCT GTGCCCAGCC CACAGATGTG GTGAAGGTCC GATTTCAGGC 780 CAGCATACAC CTCGGGCCAT CCAGGAGCGA CAGAAAATAC AGCGGGACTA TGGACGCCTA 840 25 CAGAACCATC GCCAGGGAGG AAGGAGTCAG GGGCCTGTGG AAAGGAACTT TGCCCAACAT 900 CATGAGGAAT GCTATCGTCA ACTGTGCTGA GGTGGTGACC TACGACATCC TCAAGGAGAA 960 30 GCTGCTGGAC TATCACCTGC TCACTGACAA CTTCCCCTGC CACTTTGTCT CTGCCTTTGG 1020 AGCCGCTTC TGTGCCACAG TGGTGGCCTC CCCGGTGGAC GTGGTGAAGA CCCGGTATAT 1080 1140 GAACTCACCT CCAGGCCAGT ACTTCAGCCC CCTCGACTGT ATGATAAAGA TGGTGGCCCA 35 GGAGGGCCCC ACAGCCTTCT ACAAGGGATT TACACCCTCC TTTTTGCGTT TGGGATCCTG 1200 GAACGTGGTG ATGTTCGTAA CCTATGAGCA GCTGAAACGG GCCCTGATGA AAGTCCAGAT 1260 40 GTTACGGGAA TCACCGTTTT GAACAAGACA AGAAGGCCAC TGGTAGCTAA CGTGTCCGAA 1320 ACCAGTTAAG AATGGAAGAA AACGGTGCAT CCACGCACAC ATGGACACAG ACCCACACAT 1380 GTTTACAGAA CTGTTGTTTA CTTGTTGCTG ATTCAAGAAA CAGAAGTAGA AGAGAGAGGA 1440 45 TTCTGGTCTT CACTGCCATG CCTCAAGAAC ACCTTTGTTT TGCACTGACA AGATGGAAAA 1500 TAAATTATAT TAATTTTGA AACCCATTAG GCATGCCTAA TATTTAGGCA AGAGAAAATA 1560 50 AACCAAGATA GATCCATTTG GACAAAATGG AAGGTTGGAG ACGTGTATCC CCGTGAAATC 1620 TGGTCAGATA ATGAATGATA AGCAGGAAGG ATGGCAAGCA CGGGACAGGA GGGGCCCACA 1680 ATGGAGTGGG AGATCAGCCA CGGAGCCTGG AGGGACGCCA CCCAGCAACA CAGAGCTGGC 1740 55 GACTGCAGCT GCACCATCAC ACATGCATCA TCAGCCTATT TGTAATATGT CTGCCACAGA 1800



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	GAGTCCTTTG	GGATTCTAGG	AAACCCAAGG	AACAAGAGAA	AAAACTAGAG	CCTGTGCTAA	1860
5	AGAAGCCTGC	TGGGCCCATG	TGAGGCTGGG	GTCGTAAATA	TTCCCCGACG	ACACTGAAGA	1920
,	ATCAAGAGGG	CAGCCCCCAC	TTCTCCTACA	AAATGGAGGG	AGCCATCCCT	TCCCTGTCCA	1980
	CCTCACCAGG	GGTGCTATGA	CATGCAAGTG	AGAAGCTGGG	CATGAACGCA	СТТТАТАААА	2040
10	GCAAAAGCTC	TGTGTAAATC	TAACTACAAG	GACAATGCCT	TGGGAGAGAT	TTTGTCGGGA	2100
	CAGAGAGGAG	TTGCCAGGGA	AGAAGGTTTG	AAAGATACGG	TTGTCTAGAG	GTGAGACCAA	2160
15	AGGATCCAGA	GACTTGGGGA	CCAGAGGTGA	CAGTGGATGA	CGTGAAGCCA	CAGGAGCCCC	2220
1.5	ACCCCCATGC	AGCTTTTTCC	CCACCCCCC	CACCACGCGC	TCAATCATGA	GTACCTCAAA	2280
	GGATTGTTGG	GCTTGGGGGA	AAAGAGGTGG	ATTCCTGGGC	AAGAACCTAA	AGTAGCAGGA	2340
20							

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
 - Met Val Gly Leu Lys Pro Ser Asp Val Pro Pro Thr Met Ala Val Lys

 1 5 10 15
- Phe Leu Gly Ala Gly Thr Ala Ala Cys Phe Ala Asp Leu Val Thr Phe 20 25 30
- Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Asn Gln
- Ala Val Gln Thr Ala Arg Leu Val Gln Tyr Arg Gly Val Leu Gly Thr
- Ile Leu Thr Met Val Arg Thr Glu Gly Pro Cys Ser Pro Tyr Asn Gly $65 \\ 70 \\ 75 \\ 80$
 - Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Ile Arg Ile 85 90 95
- Gly Leu Tyr Asp Ser Val Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp
 100 105 110



CATAGAATTC CAGGACTATG GTTGGAC

	Asn	Ser	Ser 115	Leu	Thr	Thr	Arg	Ile 120	Leu	Ala	Gly	Cys	Thr 125	Thr	Gly	Ala
5	Met	Ala 130	Val	Thr	Cys	Ala	Gln 135	Pro	Thr	Asp	Val	Val 140	Lys	Val	Arg	Phe
•	Gln 145	Ala	Ser	Ile	His	Leu 150	Gly	Pro	Ser	Arg	Ser 155	Asp	Arg	Lys	Tyr	Ser 160
10	Gly	Thr	Met	Asp	Ala 165	Tyr	Arg	Thr	Ile	Ala 170	Arg	Glu	Glu	Gly	Val 175	Arg
15	Gly	Leu	Trp	Lys 180	Gly	Thr	Leu	Pro	Asn 185	Ile	Met	Arg	Asn	Ala 190	Ile	Val
10	Asn	Cys	Ala 195	Glu	Val	Val	Thr	Tyr 200	Asp	Ile	Leu	Lys	Glu 205	Lys	Leu	Leu
20	Asp	Tyr 210	His	Leu	Leu	Thr	Asp 215	Asn	Phe	Pro	Cys	His 220	Phe	Val	Ser	Ala
	Phe 225	Gly	Ala	Gly	Phe	Cys 230	Ala	Thr	Val	Val	Ala 235	Ser	Pro	Val	Asp	Val 240
25	Val	Lys	Thr	Arg	Tyr 245	Met	Asn	Ser	Pro	Pro 250	Gly	Gln	Tyr	Phe	Ser 255	Pro
30	Leu	Asp	Cys	Met 260	Ile	Lys	Met	Val	Ala 265	Gln	Glu	Gly	Pro	Thr 270	Ala	Phe
	Tyr	Lys	Gly 275	Phe	Thr	Pro	Ser	Phe 280	Leu	Arg	Leu	Gly	Ser 285	Trp	Asn	Val
35	Val	Met 290	Phe	Val	Thr	Tyr	Glu 295	Gln	Leu	Lys	Arg	Ala 300	Leu	Met	Lys	Val
	Gln 305	Met	Leu	Arg	Glu	Ser 310	Pro	Phe								
40	(2) INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	0:13	:								
45	(i)	(A (B (C	UENCI LEI TYI STI	NGTH PE: 1 RANDI	: 27 nucle EDNES	base eic a SS: s	pa: acid sing!	irs								
50	(ii)	MOLI		TYI	PE: o	other	r nuc				leot:	ide"				
55	(xi)	SEQ	JENCI	E DES	SCRII	PTIO	N: SI	EQ II	ONO:	:13:						

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	(2) INFORMATION FOR SEQ ID NO:14:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
10	<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"</pre>	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
	CATTCTCGAG CTACCAGTGG CCTTCTTG	28
20	(2) INFORMATION FOR SEQ ID NO:15:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid	
23	(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
30	<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"</pre>	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15: CCCGGATCGG ACTACTAGCA	20
	(2) INFORMATION FOR SEQ ID NO:16:	2
40	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid	
4 ~	(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
45	<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "oligonucleotide"</pre>	
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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
	GGGGGGAGGG CGTGAATGTA A	23
55	(2) INFORMATION FOR SEC ID NO.17.	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1658 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

15	CCAGGAACAG	CAGAGACAAC	AGTGAATGGT	GAGGCCCGGC	CGTCAGATCC	TGCTGCTACC	60
	TAATGGAGTG	GATCCTTAGG	GTGGCCCTGC	ACTACCCAAC	CTTGGCTAGA	CGCACAGCTT	120
20	CCTCCCTGAA	CTGAAGCAAA	AGATTGCCAG	GCAAGCTCTC	TCCTCGGACC	TCCATAGGCA	180
20	GCAAAGGAAC	CAGGCCCATT	CCCCGGGACC	ATGGTTGGAC	TTCAGCCCTC	CGAAGTGCCT	240
	CCCACAACGG	TTGTGAAGTT	CCTGGGGGCC	GGCACTGCGG	CCTGTTTTGC	GGACCTCCTC	300
25	ACTTTTCCCC	TGGACACCGC	CAAGGTCCGT	CTGCAGATCC	AAGGGGAGAA	CCCAGGGGCT	360
	CAGAGCGTGC	AGTACCGCGG	TGTGCTGGGT	ACCATCCTGA	CTATGGTGCG	CACAGAGGGT	420
30	CCCCGCAGCC	CCTACAGCGG	ACTGGTCGCT	GGCCTGCACC	GCCAGATGAG	TTTTGCCTCC	480
50	ATTCGAATTG	GCCTCTACGA	CTCTGTCAAG	CAGTTCTACA	CCCCCAAGGG	AGCGGACCAC	540
	TCCAGCGTCG	CCATCAGGAT	TCTGGCAGGC	TGCACGACAG	GAGCCATGGC	AGTGACCTGC	600
35	GCCCAGCCCA	CGGATGTGGT	GAAGGTCCGA	TTTCAAGCCA	TGATACGCCT	GGGAACTGGA	660
	GGAGAGAGGA	AATACAGAGG	GACTATGGAT	GCCTACAGAA	CCATCGCCAG	GGAGGAAGGA	720
40	GTCAGGGGCC	TGTGGAAAGG	GACTTGGCCC	AACATCACAA	GAAATGCCAT	TGTCAACTGT	780
+0	GCTGAGATGG	TGACCTACGA	CATCATCAAG	GAGAAGTTGC	TGGAGTCTCA	CCTGTTTACT	840
	GACAACTTCC	CCTGTCACTT	TGTCTCTGCC	TTTGGAGCTG	GCTTCTGTGC	CACAGTGGTG	900
45	GCCTCCCCGG	TGGATGTGGT	AAAGACCCGA	TACATGAACG	CTCCCCTAGG	CAGGTACCGC	960
	AGCCCTCTGC	ACTGTATGCT	GAAGATGGTG	GCTCAGGAGG	GACCCACGGC	CTTCTACAAA	1020
50	GGATTTGTGC	CCTCCTTTCT	GCGTCTGGGA	GCTTGGAACG	TGATGATGTT	TGTAACATAT	1080
50	GAGCAACTGA	AGAGGGCCTT	AATGAAAGTC	CAGGTACTGC	GGGAATCTCC	GTTTTGAACA	1140
	AGGCAAGCAG	GCTGCCTGGA	ACAGAACAAA	GCGTCTCTGC	CCTGGGGACA	CAGGCCCACA	1200
55	CGGTCCAGAA	CCCTGCACTG	CTGCTGACAC	GAGAAACTGA	ACTAAAAGAG	GAGAGTTTTA	1260



	GTCCTCCG	TG T	TTCG'	rcct <i>i</i>	AAA	ACAC	CTCT	GTT.	PTGC?	ACT (GACC'	IGAT	GG G	AAAT	AAAT:	Г	1320
	АТАТТААТ	TT T	TAAA	CCCTI	TC	CGGT	rgga	TGC	CTAAC	CAT	TTAG	3CAA	GA G	ACAA	CAAAC	3	1380
5	AAAACCAG	AG T	CAAC	rccci	TG	YTAAA	GTAG	GAA!	PAAA	GGA '	TGCA:	TAAT	AA AA	CAGG	AAAGO	3	1440
	CACAGGTT	TT G	AGAA	GATC	A GC	CCAC	AGTG	TTG	rcct.	rĠA .	ATCA	AACA	AA A	rggt	CGGA	3	1500
10	GAACCCTT	CG G	GTTC	AGCAC	C AA	AGAG	GTGA	CTA	CAGC	CTT	TTGG'	rcaco	CA G	ATGA	CTCCC	3	1560
10	CCCCTTTG	TA A'	TGAG'	rctgo	CA	AGTA	GACT	CTA	rcaa	GAT '	rctg	GGA	AA G	GAGA	AAGA	A	1620
	CACATTGA	CC T	GCCC	GGCC	GC	CGCT	CGAG	CCC	ratg?	A							1658
15	(2) INFO	RMAT:	ION I	FOR S	SEQ :	ID N	0:18	:									
20	(i)	(B (C) LEI) TYI) STI	E CHANGTH: PE: & RANDI POLOC	308 mine EDNE	8 am: cac: SS: s	ino a id sing:	acid	5								
25	(ii)	MOLI (A		E TYI							leot	ide"					
30	(xi)	SEQ	U EN CI	E DES	SCRI	PTIO	N: SI	EQ II	ONO:	:18:							
	Met 1	Val	Gly	Leu	Gln 5	Pro	Ser	Glu	Val	Pro 10	Pro	Thr	Thr	Val	Val 15	Lys	
35	Phe	Leu	Gly	Ala 20	Gly	Thr	Ala	Ala	Cys 25	Phe	Ala	Asp	Leu	Leu 30	Thr	Phe	
	Pro	Leu	Asp 35	Thr	Ala	Lys	Val	Arg 40	Leu	Gln	Ile	Gln	Gly 45	Glu	Asn	Pro	
40	Gly	A la 50	Gln	Ser	Val	Gln	_	Arg	_			Gly 60	Thr	Ile	Leu	Thr	
45	M et 65	Val	Arg	Thr	Glu	Gly 70	Pro	Arg	Ser	Pro	Tyr 75	Ser	Gly	Leu	Val	Ala 80	
4)	Gly	Leu	His	Arg	Gln 85	Met	Ser	Phe	Ala	Ser 90	Ile	Arg	Ile	Gly	Leu 95	Tyr	
50	Asp	Ser	Val	Lys 100	Gln	Phe	Tyr	Thr	Pro 105	Lys	Gly	Ala	Asp	His 110	Ser	Ser	
	Val	Ala	Ile	Arg	Ile	Leu	Ala	Gly	Cys	Thr	Thr	Gly	Ala	Met	Ala	Val	



Thr Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe Gln Ala Met 130 135 140

		Ile 145	Arg	Leu	Gly	Thr	Gly 150	Gly	Glu	Arg	Lys	Tyr 155	Arg	Gly	Thr	Met	Asp 160	
5		Ala	Tyr	Arg	Thr	Ile 165	Ala	Arg	Glu	Glu	Gly 170	Val	Arg	Gly	Leu	Trp 175	Lys	
10		Gly	Thr	Trp	Pro 180	Asn	Ile	Thr	Arg	Asn 185	Ala	Ile	Val	Asn	Cys 190	Ala	Glu	
10		Met	Val	Thr 195	Tyr	Asp	Ile	Ile	Lys 200	Glu	Lys	Leu	Leu	Glu 205	Ser	His	Leu	
15		Phe	Thr 210	Asp	Asn	Phe	Pro	Cys 215	His	Phe	Val	Ser	Ala 220	Phe	Gly	Ala	Gly	
		Phe . 225	Cys	Ala	Thr	Val	Val 230	Ala	Ser	Pro	Val	Asp 235	Val	Val	Lys	Thr	A rg 240	
20		Tyr	Met	Asn	Ala	Pro 245	Leu	Gly	Arg	Tyr	Arg 250	Ser	Pro	Leu	His	Cys 255	Met	
25		Leu	Lys	Met	Val 260	Ala	Gln	Glu	Gly	Pro 265	Thr	Ala	Phe	Tyr	Lys 270	Gly	Phe	
		Val	Pro	Ser 275	Phe	Leu	Arg	Leu	Gly 280	Ala	Trp	Asn	Va1	Met 285	Met	Phe	Val	
30		Thr	Tyr 290	Glu	Gln	Leu	Lys	Arg 295	Ala	Leu	Met	Lys	Val 300	Gln	Val	Leu	Arg	
		Glu 305	Ser	Pro	Phe													
35	(2)			ION I														
40			(A) (B) (C)	LENCE LENCE TYI STI TOI	NGTH: PE: r RANDE	: 17 nucle EDNES	base eic a SS: s	e pai acid singl	irs									
45		(ii)		ECULE DES								e ol	ligor	nucle	eotio	de"		
50		(xi)				CRIE	OIT	N: SE	EQ II	NO:	19:							
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55	(4)			JENCE														
		`-,		LEN														



	(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
5	<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "degenerate oligonucleotide"</pre>	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
	CAGCCCACNG ANGTNGT	17
15	(2) INFORMATION FOR SEQ ID NO:21:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
25	<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "degenerate oligonucleotide"</pre>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
30	TTCACCACRT CNACNGG	17